Maps

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Maps

Import Data

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library(ggmap)
```

```
## Google's Terms of Service: https://cloud.google.com/maps-platform/terms/.

## Please cite ggmap if you use it! See citation("ggmap") for details.
```

```
library(maps)
library(mapdata)
library(usmap)
data <- read.csv("./Project 02/nwCrow_bloodParasites_alaska_smith_2007_2008/nwCrow_sampling_alaska_smith
data_2 <- read.csv("./Project 02/nwCrow_bloodParasites_alaska_smith_2007_2008/nwCrow_bloodParasites_ala
de <- merge(data, data_2, by=0, all=TRUE)
head(de)
```

```
##   Row.names Field.ID      DATE  LOC   LAT    LONG SEX AGE AKD TARSUS WING MASS
## 1         1    75001 3/20/2007 SEWA 60.11 -149.44   1   1   1   55.8  283  448
## 2        10    75010 3/22/2007 KENA 60.55 -151.23   2   1   0   48.6  271  390
## 3       100    75100 3/12/2008 VALD 61.12 -146.35   2   1   0   44.6  264  317
## 4       101    86701 3/12/2008 VALD 61.12 -146.35   2   1   0   47.1  269  343
```

```
## 5       102    86702 3/12/2008 VALD 61.12 -146.35   2   2   0   52.2  291  415
## 6       103    86703 3/12/2008 VALD 61.12 -146.35   1   2   0   47.0  266  325
##   Extraction.. LEUC1 LEUC2 HAEM1 HAEM2 PLAS1 PLAS2 Leuc_GenBank_Accession
## 1      NOCR001     0     0     0     0     0     0
## 2      NOCR010     0     0     0     0     0     0
## 3      NOCR100     1     1     0     0     0     0              MG765394
## 4      NOCR101     0     0     0     0     0     0
## 5      NOCR102     1     0     0     0     0     0              MG765394
## 6      NOCR103     1     1     0     0     0     0              MG765394
##   Haem_GenBank_Accession Plas_GenBank_Accession
## 1
## 2
## 3
## 4
## 5
## 6
```

Filter Columns and N/A Values

```
de <- de[,c(6,5,2,4,7,8,9,10,11,12,13,14,16,18)]
de<-de[complete.cases(de),]
head(de)
```

```
##      LONG   LAT Field.ID  LOC SEX AGE AKD TARSUS WING MASS Extraction.. LEUC1
## 1 -149.44 60.11    75001 SEWA   1   1   1   55.8  283  448      NOCR001     0
## 2 -151.23 60.55    75010 KENA   2   1   0   48.6  271  390      NOCR010     0
## 3 -146.35 61.12    75100 VALD   2   1   0   44.6  264  317      NOCR100     1
## 4 -146.35 61.12    86701 VALD   2   1   0   47.1  269  343      NOCR101     0
## 5 -146.35 61.12    86702 VALD   2   2   0   52.2  291  415      NOCR102     1
## 6 -146.35 61.12    86703 VALD   1   2   0   47.0  266  325      NOCR103     1
##   HAEM1 PLAS1
## 1     0     0
## 2     0     0
## 3     0     0
## 4     0     0
## 5     0     0
## 6     0     0
```

```
de_2 <- de[,c(1,2,4)]
head(de_2)
```

```
##      LONG   LAT  LOC
## 1 -149.44 60.11 SEWA
## 2 -151.23 60.55 KENA
## 3 -146.35 61.12 VALD
## 4 -146.35 61.12 VALD
## 5 -146.35 61.12 VALD
## 6 -146.35 61.12 VALD
```

```
LEUC1_Count <- de %>% group_by(LOC)  %>% count(LEUC1) %>% filter(LEUC1==1)
LEUC1_Count_2 <- merge(LEUC1_Count, de_2, by.x='LOC', by.y='LOC', all=TRUE)
LEUC1_Count_2 <- LEUC1_Count_2[,c(4,5,1,3)]
head(LEUC1_Count_2)
```

```
##      LONG   LAT  LOC  n
## 1 -135.44 59.23 HAIN 15
## 2 -135.44 59.23 HAIN 15
## 3 -135.44 59.23 HAIN 15
## 4 -135.44 59.23 HAIN 15
## 5 -135.44 59.23 HAIN 15
## 6 -135.44 59.23 HAIN 15
```

```
HAEM1_Count <- de %>% group_by(LOC)  %>% count(HAEM1) %>% filter(HAEM1==1)
HAEM1_Count_2 <- merge(HAEM1_Count, de_2, by.x='LOC', by.y='LOC', all=TRUE)
HAEM1_Count_2 <- HAEM1_Count_2[,c(4,5,1,3)]
head(HAEM1_Count_2)
```

```
##      LONG   LAT  LOC  n
## 1 -135.44 59.23 HAIN 21
## 2 -135.44 59.23 HAIN 21
## 3 -135.44 59.23 HAIN 21
## 4 -135.44 59.23 HAIN 21
## 5 -135.44 59.23 HAIN 21
## 6 -135.44 59.23 HAIN 21
```

```
PLAS1_Count <- de %>% group_by(LOC)  %>% count(PLAS1) %>% filter(PLAS1==1)
PLAS1_Count_2 <- merge(PLAS1_Count, de_2, by.x='LOC', by.y='LOC', all=TRUE)
PLAS1_Count_2 <- PLAS1_Count_2[,c(4,5,1,3)]
head(PLAS1_Count_2)
```

```
##      LONG   LAT  LOC  n
## 1 -135.44 59.23 HAIN NA
## 2 -135.44 59.23 HAIN NA
## 3 -135.44 59.23 HAIN NA
## 4 -135.44 59.23 HAIN NA
## 5 -135.44 59.23 HAIN NA
## 6 -135.44 59.23 HAIN NA
```

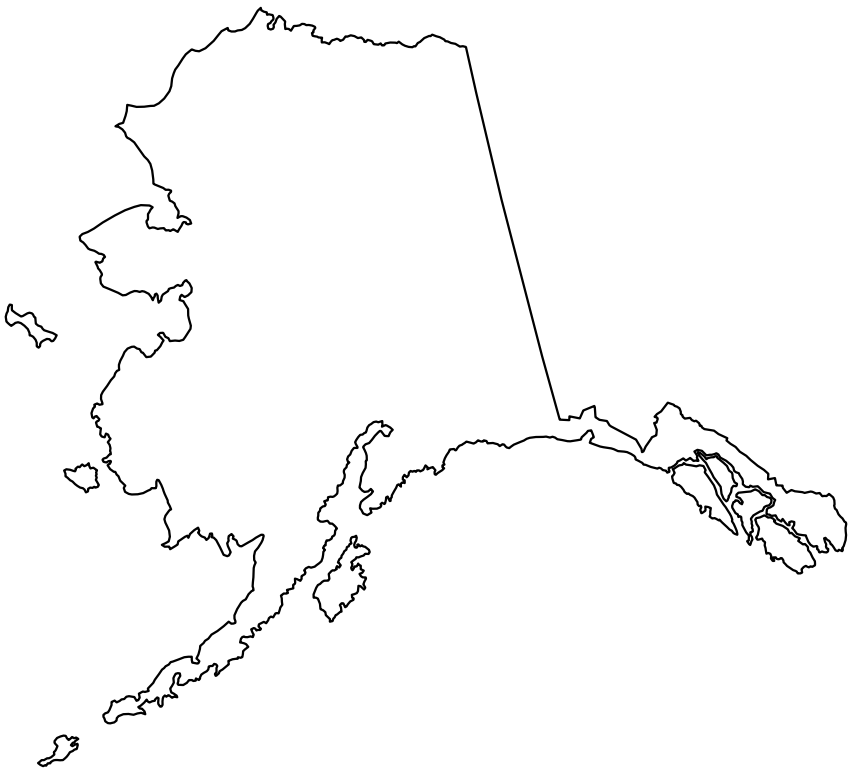
Basic Plot

```
plot_usmap("states", include=c("AK"))
```

```
## Warning: Use of `map_df$x` is discouraged. Use `x` instead.
```

```
## Warning: Use of `map_df$y` is discouraged. Use `y` instead.
```

```
## Warning: Use of `map_df$group` is discouraged. Use `group` instead.
```



```
de <- data.frame(de)
transformed_data <- usmap_transform(de)
head(transformed_data)
```

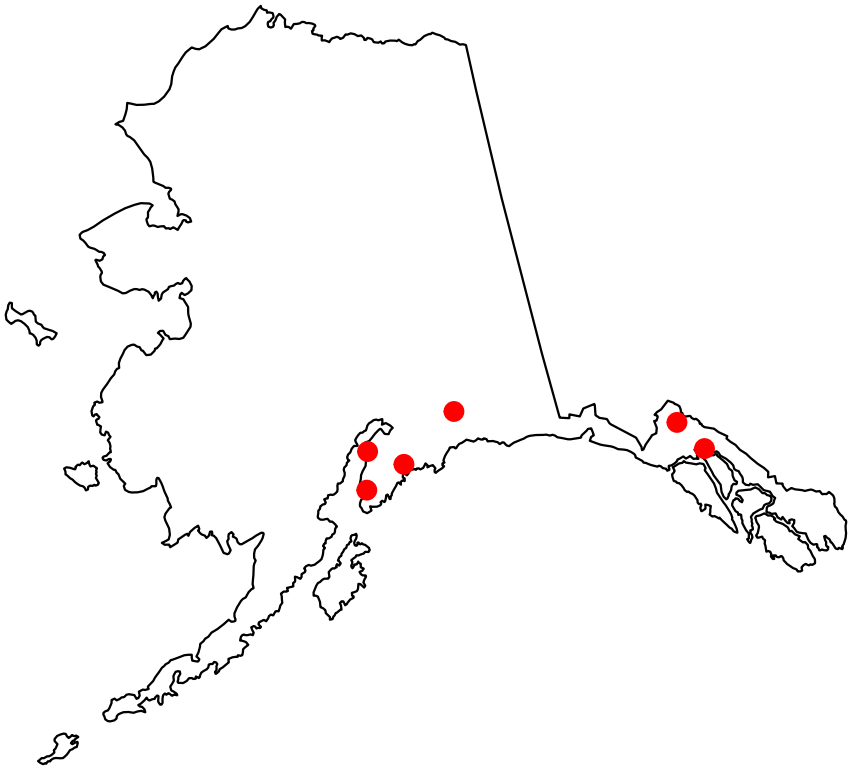
```
##      LONG   LAT Field.ID  LOC SEX AGE AKD TARSUS WING MASS Extraction.. LEUC1
## 1 -134.64 58.38     6151 JUNE   1   1   0   49.3  282  415      NOCR169     0
## 2 -135.44 59.23    75034 HAIN   2   2   0   44.6  266  400      NOCR034     0
## 3 -151.54 59.64    75076 HOME   1   1   0   47.1  272  366      NOCR076     1
## 4 -149.44 60.11    75008 SEWA   2   2   0   48.3  256  347      NOCR008     0
## 5 -151.23 60.55    75009 KENA   1   2   0   50.0  274  372      NOCR009     1
## 6 -146.35 61.12    75099 VALD   1   2   0   47.8  272  357      NOCR099     1
##   HAEM1 PLAS1     LONG.1    LAT.1
## 1     1     0  -780707.5 -2081990
## 2     1     0  -813924.5 -2050463
## 3     0     0 -1187689.1 -2132081
## 4     1     0 -1142899.7 -2100989
## 5     1     0 -1186683.3 -2085527
## 6     0     1 -1082645.1 -2037269
```

```
plot_usmap("states", include=c("AK")) +
  geom_point(data = transformed_data,
             aes(x = LONG.1, y = LAT.1, group=LOC),
             color = "red",
             size = 3)
```

```
## Warning: Use of `map_df$x` is discouraged. Use `x` instead.
```

```
## Warning: Use of `map_df$y` is discouraged. Use `y` instead.

## Warning: Use of `map_df$group` is discouraged. Use `group` instead.
```

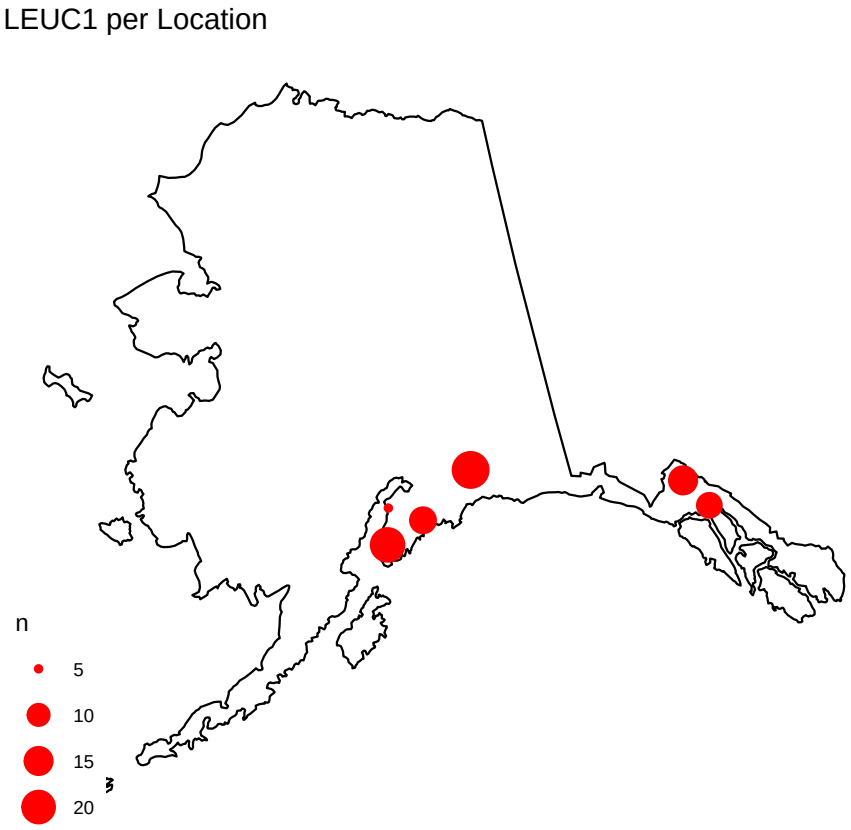


```
LEUC1_Count_2 <- data.frame(LEUC1_Count_2)
transformed_data_LEUC1 <- usmap_transform(LEUC1_Count_2)
plot_usmap("states", include=c("AK")) +
  geom_point(data = transformed_data_LEUC1,
             aes(x = LONG.1, y = LAT.1, group=LOC, size=n),
             color = "red") +
  ggtitle("LEUC1 per Location")
```

```
## Warning: Use of `map_df$x` is discouraged. Use `x` instead.

## Warning: Use of `map_df$y` is discouraged. Use `y` instead.

## Warning: Use of `map_df$group` is discouraged. Use `group` instead.
```



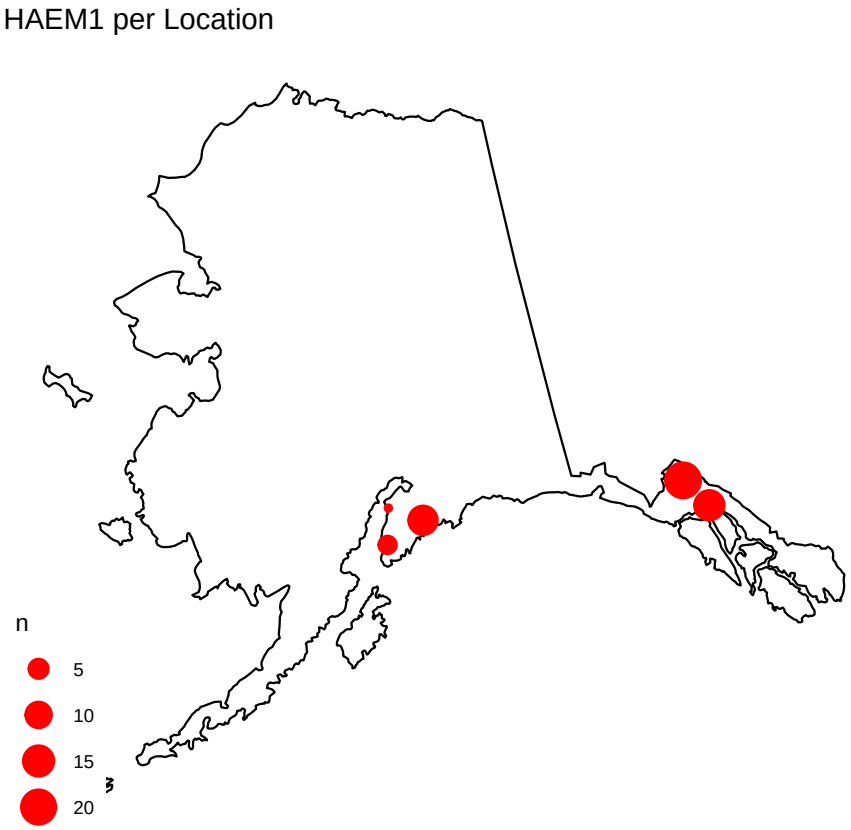

```
HAEM1_Count_2 <- data.frame(HAEM1_Count_2)
transformed_data_HAEM1 <- usmap_transform(HAEM1_Count_2)
plot_usmap("states", include=c("AK")) +
  geom_point(data = transformed_data_HAEM1,
             aes(x = LONG.1, y = LAT.1, group=LOC, size=n),
             color = "red") +
  ggtitle("HAEM1 per Location")
```

```
## Warning: Use of `map_df$x` is discouraged. Use `x` instead.

## Warning: Use of `map_df$y` is discouraged. Use `y` instead.

## Warning: Use of `map_df$group` is discouraged. Use `group` instead.

## Warning: Removed 1 rows containing missing values (geom_point).
```




```
PLAS1_Count_2 <- data.frame(PLAS1_Count_2)
transformed_data_PLAS1 <- usmap_transform(PLAS1_Count_2)
plot_usmap("states", include=c("AK")) +
  geom_point(data = transformed_data_PLAS1,
             aes(x = LONG.1, y = LAT.1, group=LOC, size=n),
             color = "red") +
  ggtitle("PLAS1 per Location")
```

```
## Warning: Use of `map_df$x` is discouraged. Use `x` instead.

## Warning: Use of `map_df$y` is discouraged. Use `y` instead.

## Warning: Use of `map_df$group` is discouraged. Use `group` instead.

## Warning: Removed 1 rows containing missing values (geom_point).
```

PLAS1 per Location